

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (I) APPLICANT: DUAN, D. ROXANNE
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CONAWAY, RONALD C.
- (ii) TITLE OF INVENTION: ELL2, A New Member of an ELL Family of RNA Polymerase II Elongation Factors
- (iii) NUMBER OF SEQUENCES: 34
- (iv) CORRESPONDENCE ADDRESS:
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(C) CITY: WASHINGTON
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(E) COUNTRY: USA
(F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: To be assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/038,447
(B) FILING DATE: 19-FEB-1997
- (viii) ATTORNEY/AGENT INFORMATION:
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(C) REFERENCE/DOCKET NUMBER: 1488.0880001
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 94..2013

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAGTGGCGGC	GGGTGCAGAA	GCCCAAGCAG	CGCGGCCGCA	GTGGAGGCTA	GAGCCGGAGC	60
GGCGGCCGGCG	GCAGCACCCC	GGGGAGGTTT	AAG ATG GCG GCG GGG GGG ACA GGG			114
			Met Ala Ala Gly Gly Thr Gly			
			1	5		
GGC CTG CGG GAG GAG CAG CGC TAT GGG CTG TCG TGC GGA CGG CTG GGG						162
Gly Leu Arg Glu Glu Gln Arg Tyr Gly Leu Ser Cys Gly Arg Leu Gly						
10	15	20				
CAG GAC AAC ATC ACC GTA CTG CAT GTG AAG CTC ACC GAG ACG GCG ATC						210
Gln Asp Asn Ile Thr Val Leu His Val Lys Leu Thr Glu Thr Ala Ile						
25	30	35				
CGG GCG CTC GAG ACT TAC CAG AGC CAC AAG AAT TTA ATT CCT TTT CGA						258
Arg Ala Leu Glu Thr Tyr Gln Ser His Lys Asn Leu Ile Pro Phe Arg						
40	45	50	55			
CCT TCA ATC CAG TTC CAA GGA CTC CAC GGG CTT GTC AAA ATT CCC AAA						306
Pro Ser Ile Gln Phe Gln Gly Leu His Gly Leu Val Lys Ile Pro Lys						
60	65	70				
AAT GAT CCC CTC AAT GAA GTT CAT AAC TTT AAC TTT TAT TTG TCA AAT						354
Asn Asp Pro Leu Asn Glu Val His Asn Phe Asn Phe Tyr Leu Ser Asn						
75	80	85				
GTG GGC AAA GAC AAC CCT CAG GGC AGC TTT GAC TGC ATC CAG CAA ACA						402
Val Gly Lys Asp Asn Pro Gln Gly Ser Phe Asp Cys Ile Gln Gln Thr						
90	95	100				
TTC TCC AGC TCT GGA GCC TCC CAG CTC AAT TGC CTG GGA TTT ATA CAA						450
Phe Ser Ser Ser Gly Ala Ser Gln Leu Asn Cys Leu Gly Phe Ile Gln						
105	110	115				
GAT AAA ATT ACA GTG TGT GCA ACA AAC GAC TCG TAT CAG ATG ACA CGA						498
Asp Lys Ile Thr Val Cys Ala Thr Asn Asp Ser Tyr Gln Met Thr Arg						
120	125	130	135			
GAA AGA ATG ACC CAG GCA GAG GAG GAA TCC CGC AAC CGA AGC ACA AAA						546
Glu Arg Met Thr Gln Ala Glu Glu Ser Arg Asn Arg Ser Thr Lys						
140	145	150				
GTT ATC AAA CCC GGT GGA CCA TAT GTA GGG AAA AGA GTG CAA ATT CGG						594
Val Ile Lys Pro Gly Gly Pro Tyr Val Gly Lys Arg Val Gln Ile Arg						
155	160	165				
AAA GCA CCT CAA GCT GTT TCA GAT ACA GTT CCT GAG AGG AAA AGG TCA						642
Lys Ala Pro Gln Ala Val Ser Asp Thr Val Pro Glu Arg Lys Arg Ser						
170	175	180				
ACC CCC ATG AAC CCT GCA AAT ACA ATT CGA AAG ACA CAT AGC AGC AGC						690
Thr Pro Met Asn Pro Ala Asn Thr Ile Arg Lys Thr His Ser Ser Ser						
185	190	195				
ACC ATC TCT CAG AGG CCA TAC AGG GAC AGG GTG ATT CAC TTA CTG GCC						738
Thr Ile Ser Gln Arg Pro Tyr Arg Asp Arg Val Ile His Leu Leu Ala						
200	205	210	215			
CTG AAG GCC TAC AAG AAA CCG GAG CTA CTT GCT AGA CTC CAG AAA GAT						786

Leu	Lys	Ala	Tyr	Lys	Lys	Pro	Glu	Leu	Leu	Ala	Arg	Leu	Gln	Lys	Asp			
				220				225				230						
GGT	GTC	AAT	CAA	AAA	GAC	AAG	AAC	TCC	CTG	GGA	GCA	ATT	CTG	CAA	CAG	834		
Gly	Val	Asn	Gln	Lys	Asp	Lys	Asn	Ser	Leu	Gly	Ala	Ile	Leu	Gln	Gln			
				235				240				245						
GTA	GCC	AAT	CTG	AAT	TCT	AAG	GAC	CTC	TCA	TAT	ACC	TTA	AAG	GAT	TAT	882		
Val	Ala	Asn	Leu	Asn	Ser	Lys	Asp	Leu	Ser	Tyr	Thr	Leu	Lys	Asp	Tyr			
				250				255				260						
GTT	TTT	AAA	GAG	CTT	CAA	AGA	GAC	TGG	CCT	GGA	TAC	AGT	GAA	ATA	GAC	930		
Val	Phe	Lys	Glu	Leu	Gln	Arg	Asp	Trp	Pro	Gly	Tyr	Ser	Glu	Ile	Asp			
				265				270				275						
AGA	CGG	TCA	TTG	GAG	TCA	GTG	CTC	TCT	AGA	AAA	CTA	AAT	CCG	TCT	CAG	978		
Arg	Arg	Ser	Leu	Glu	Ser	Val	Leu	Ser	Arg	Lys	Leu	Asn	Pro	Ser	Gln			
				280				285				290				295		
G	AAT	GCT	ACA	GGC	ACC	AGC	CGT	TCA	GAA	TCT	CCT	GTA	TGT	TCT	AGT	AGA	1026	
G	Asn	Ala	Thr	Gly	Thr	Ser	Arg	Ser	Glu	Ser	Pro	Val	Cys	Ser	Ser	Arg		
				300				305				310						
G	GAT	GCT	GTA	TCT	TCT	CCT	CAG	AAA	CGG	CTT	TTG	GAT	TCA	GAG	TTT	ATT	1074	
G	Asp	Ala	Val	Ser	Ser	Pro	Gln	Lys	Arg	Leu	Leu	Asp	Ser	Glu	Phe	Ile		
				315				320				325						
G	=	GAT	CCT	TTA	ATG	AAT	AAA	AAA	GCC	CGA	ATA	TCT	CAC	CTG	ACG	AAC	AGA	1122
G	Asp	Pro	Leu	Met	Asn	Lys	Lys	Ala	Arg	Ile	Ser	His	Leu	Thr	Asn	Arg		
				330				335				340						
G	G	GTA	CCA	CCA	ACA	CTA	AAT	GGT	CAT	TTG	AAT	CCC	ACC	AGT	GAA	AAA	TCG	1170
G	Val	Pro	Pro	Thr	Leu	Asn	Gly	His	Leu	Asn	Pro	Thr	Ser	Glu	Lys	Ser		
				345				350				355						
G	G	GCT	GCA	GGC	CTC	CCA	CTG	CCC	CCT	GCG	GCT	GCT	GCC	ATC	CCC	ACC	CCT	1218
G	Ala	Ala	Gly	Leu	Pro	Leu	Pro	Pro	Ala	Ala	Ala	Ala	Ile	Pro	Thr	Pro		
				360				365				370					375	
G	G	CCA	CCG	CTG	CCT	TCA	ACC	TAT	CTG	CCC	ATC	TCA	CAT	CCT	CCT	CAG	ATT	1266
G	Pro	Pro	Leu	Pro	Ser	Thr	Tyr	Leu	Pro	Ile	Ser	His	Pro	Pro	Gln	Ile		
				380				385				390						
G	G	GTA	AAT	TCT	AAC	TCC	AAC	TCC	CCT	AGC	ACT	CCA	GAA	GGC	CGG	GGG	ACT	1314
G	Val	Asn	Ser	Asn	Ser	Asn	Ser	Pro	Ser	Thr	Pro	Glu	Gly	Arg	Gly	Thr		
				395				400				405						
G	G	CAA	GAC	CTA	CCT	GTT	GAC	AGT	TTT	AGT	CAA	AAC	GAT	AGT	ATC	TAT	GAG	1362
G	Gln	Asp	Leu	Pro	Val	Asp	Ser	Phe	Ser	Gln	Asn	Asp	Ser	Ile	Tyr	Glu		
				410				415				420						
G	G	GAC	CAG	CAA	GAC	AAA	TAT	ACC	TCT	AGG	ACT	TCT	CTG	GAA	ACC	TTA	CCC	1410
G	Asp	Gln	Gln	Asp	Lys	Tyr	Thr	Ser	Arg	Thr	Ser	Leu	Glu	Thr	Leu	Pro		
				425				430				435						
G	G	CCT	GGT	TCC	CTA	CTA	AAG	TGT	CCA	AAG	CCT	ATG	GAA	GAA	AAC	CAT	1458	
G	Pro	Gly	Ser	Val	Leu	Leu	Lys	Cys	Pro	Lys	Pro	Met	Glu	Glu	Asn	His		
				440				445				450					455	
G	G	TCA	ATG	TCT	CAC	AAA	AAG	TCC	AAA	AAG	AAG	TCT	AAA	AAA	CAT	AAG	GAA	1506
G	Ser	Met	Ser	His	Lys	Lys	Ser	Lys	Lys	Ser	Lys	Lys	Ser	Lys	Lys	His	Glu	
				460				465				470						

AAG GAC CAA ATA AAA AAG CAC GAC ATT GAG ACT ATT GAG GAA AAG GAG Lys Asp Gln Ile Lys Lys His Asp Ile Glu Thr Ile Glu Glu Lys Glu 475 480 485	1554
GAA GAT CTT AAG AGA GAA GAG GAA ATT GCC AAG CTA AAT AAC TCC AGT Glu Asp Leu Lys Arg Glu Glu Glu Ile Ala Lys Leu Asn Asn Ser Ser 490 495 500	1602
CCA AAT TCC AGT GGA GGA GTT AAA GAG GAT TGC ACT GCC TCC ATG GAA Pro Asn Ser Ser Gly Gly Val Lys Glu Asp Cys Thr Ala Ser Met Glu 505 510 515	1650
CCT TCA GCA ATT GAA CTC CCA GAT TAT TTG ATA AAA TAT ATC GCT ATC Pro Ser Ala Ile Glu Leu Pro Asp Tyr Leu Ile Lys Tyr Ile Ala Ile 520 525 530 535	1698
GTC TCC TAT GAG CAA CGC CAG AAT TAT AAG GAT GAC TTC AAT GCA GAG Val Ser Tyr Glu Gln Arg Gln Asn Tyr Lys Asp Asp Phe Asn Ala Glu 540 545 550	1746
TAT GAT GAG TAC AGA GCT TTG CAT GCC AGG ATG GAG ACT GTA GCT AGA Tyr Asp Glu Tyr Arg Ala Leu His Ala Arg Met Glu Thr Val Ala Arg 555 560 565	1794
AGA TTT ATC AAA CTA GAT GCA CAA AGA AAG CGC CTT TCT CCA GGC TCA Arg Phe Ile Lys Leu Asp Ala Gln Arg Lys Arg Leu Ser Pro Gly Ser 570 575 580	1842
AAA GAG TAT CAG AAT GTT CAT GAA GAA GTC TTA CAA GAA TAT CAG AAG Lys Glu Tyr Gln Asn Val His Glu Glu Val Leu Gln Glu Tyr Gln Lys 585 590 595	1890
ATA AAG CAG TCT AGT CCC AAT TAC CAT GAA GAA AAA TAC AGA TGT GAA Ile Lys Gln Ser Ser Pro Asn Tyr His Glu Glu Lys Tyr Arg Cys Glu 600 605 610 615	1938
TAT CTT CAT AAC AAG CTG GCT CAC ATC AAA AGG CTA ATA GGT GAA TTT Tyr Leu His Asn Lys Leu Ala His Ile Lys Arg Leu Ile Gly Glu Phe 620 625 630	1986
GAC CAA CAG CAA GCA GAG TCA TGG TCC TAGAACTCTG CTTGGACCAG Asp Gln Gln Ala Glu Ser Trp Ser 635 640	2033
AAGATGTGAA TAAACTTAAG CTTATTATT TAAAATTCCA AATGAGTTGC TCTAGATTCT AAAAAGGTGA AACTTGGCT GTTGAAAGTT TCAGTATTAG TAAACT	2093
	2139

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 640 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Ala Gly Gly Thr Gly Gly Leu Arg Glu Glu Gln Arg Tyr Gly
1 5 10 15

Leu Ser Cys Gly Arg Leu Gly Gln Asp Asn Ile Thr Val Leu His Val
20 25 30

Lys Leu Thr Glu Thr Ala Ile Arg Ala Leu Glu Thr Tyr Gln Ser His
35 40 45

Lys Asn Leu Ile Pro Phe Arg Pro Ser Ile Gln Phe Gln Gly Leu His
50 55 60

Gly Leu Val Lys Ile Pro Lys Asn Asp Pro Leu Asn Glu Val His Asn
65 70 75 80

Phe Asn Phe Tyr Leu Ser Asn Val Gly Lys Asp Asn Pro Gln Gly Ser
85 90 95

Phe Asp Cys Ile Gln Gln Thr Phe Ser Ser Ser Gly Ala Ser Gln Leu
100 105 110

Asn Cys Leu Gly Phe Ile Gln Asp Lys Ile Thr Val Cys Ala Thr Asn
115 120 125

Asp Ser Tyr Gln Met Thr Arg Glu Arg Met Thr Gln Ala Glu Glu Glu
130 135 140

Ser Arg Asn Arg Ser Thr Lys Val Ile Lys Pro Gly Gly Pro Tyr Val
145 150 155 160

Gly Lys Arg Val Gln Ile Arg Lys Ala Pro Gln Ala Val Ser Asp Thr
165 170 175

Val Pro Glu Arg Lys Arg Ser Thr Pro Met Asn Pro Ala Asn Thr Ile
180 185 190

Arg Lys Thr His Ser Ser Ser Thr Ile Ser Gln Arg Pro Tyr Arg Asp
195 200 205

Arg Val Ile His Leu Leu Ala Leu Lys Ala Tyr Lys Lys Pro Glu Leu
210 215 220

Leu Ala Arg Leu Gln Lys Asp Gly Val Asn Gln Lys Asp Lys Asn Ser
225 230 235 240

Leu Gly Ala Ile Leu Gln Gln Val Ala Asn Leu Asn Ser Lys Asp Leu
245 250 255

Ser Tyr Thr Leu Lys Asp Tyr Val Phe Lys Glu Leu Gln Arg Asp Trp
260 265 270

Pro Gly Tyr Ser Glu Ile Asp Arg Arg Ser Leu Glu Ser Val Leu Ser
275 280 285

Arg Lys Leu Asn Pro Ser Gln Asn Ala Thr Gly Thr Ser Arg Ser Glu
290 295 300

Ser Pro Val Cys Ser Ser Arg Asp Ala Val Ser Ser Pro Gln Lys Arg
305 310 315 320

Leu Leu Asp Ser Glu Phe Ile Asp Pro Leu Met Asn Lys Lys Ala Arg
325 330 335

Ile Ser His Leu Thr Asn Arg Val Pro Pro Thr Leu Asn Gly His Leu
340 345 350

Asn Pro Thr Ser Glu Lys Ser Ala Ala Gly Leu Pro Pro Pro Ala
355 360 365

Ala Ala Ala Ile Pro Thr Pro Pro Pro Leu Pro Ser Thr Tyr Leu Pro
370 375 380 400

Ile Ser His Pro Pro Gln Ile Val Asn Ser Asn Ser Asn Ser Pro Ser
385 390 395 400

Thr Pro Glu Gly Arg Gly Thr Gln Asp Leu Pro Val Asp Ser Phe Ser
405 410 415

Gln Asn Asp Ser Ile Tyr Glu Asp Gln Gln Asp Lys Tyr Thr Ser Arg
420 425 430

Thr Ser Leu Glu Thr Leu Pro Pro Gly Ser Val Leu Leu Lys Cys Pro
435 440 445

Lys Pro Met Glu Glu Asn His Ser Met Ser His Lys Lys Ser Lys Lys
450 455 460

Lys Ser Lys Lys His Lys Glu Lys Asp Gln Ile Lys Lys His Asp Ile
465 470 475 480

Glu Thr Ile Glu Glu Lys Glu Glu Asp Leu Lys Arg Glu Glu Glu Ile
485 490 495

Ala Lys Leu Asn Asn Ser Ser Pro Asn Ser Ser Gly Gly Val Lys Glu
500 505 510

Asp Cys Thr Ala Ser Met Glu Pro Ser Ala Ile Glu Leu Pro Asp Tyr
515 520 525

Leu Ile Lys Tyr Ile Ala Ile Val Ser Tyr Glu Gln Arg Gln Asn Tyr
530 535 540

Lys Asp Asp Phe Asn Ala Glu Tyr Asp Glu Tyr Arg Ala Leu His Ala
545 550 555 560

Arg Met Glu Thr Val Ala Arg Arg Phe Ile Lys Leu Asp Ala Gln Arg
565 570 575

Lys Arg Leu Ser Pro Gly Ser Lys Glu Tyr Gln Asn Val His Glu Glu
580 585 590

Val Leu Gln Glu Tyr Gln Lys Ile Lys Gln Ser Ser Pro Asn Tyr His
595 600 605

Glu Glu Lys Tyr Arg Cys Glu Tyr Leu His Asn Lys Leu Ala His Ile
610 615 620

Lys Arg Leu Ile Gly Glu Phe Asp Gln Gln Ala Glu Ser Trp Ser
625 630 635 640

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAATTAACCC TCATAAAGGG AAC

23

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAAAGTTCA CCTTTAGAA TCTAGAGCAA CTC

33

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAGGTGTCGA CGAGGAGCAG CGCTATGGGC TGTCGTGCGG AC

42

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTGTGGATCC TCATCACTAG GACCATGACT CTGCTTGCTG TTG

43

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 621 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Ala Leu Lys Glu Asp Arg Ser Tyr Gly Leu Ser Gly Gly Arg
1 5 10 15

Val Ser Asp Gly Ser Lys Val Ser Val Phe His Val Lys Leu Thr Asp
20 25 30

Ser Ala Ile Arg Ala Phe Glu Ser Tyr Arg Ala Arg Gln Asp Ser Val
35 40 45

Ser Leu Arg Pro Ser Ile Arg Phe Gln Gly Ser Gln Gly His Ile Ser
50 55 60

Ile Pro Gln Pro Asp Cys Pro Ala Glu Ala Arg Thr Phe Ser Phe Tyr
65 70 75 80

Leu Ser Asn Ile Gly Arg Asp Asn Pro Gln Gly Ser Phe Asp Cys Ile
85 90 95

Gln Gln Tyr Val Ser Ser His Gly Glu Val His Leu Asp Cys Leu Gly
100 105 110

Ser Ile Gln Asp Lys Ile Thr Val Cys Ala Thr Asp Asp Ser Tyr Gln
115 120 125

Lys Ala Arg Gln Ser Met Ala Gln Ala Glu Glu Ile Arg Ser Arg
130 135 140

Ser Ala Ile Val Ile Lys Ala Gly Gly Arg Tyr Leu Gly Lys Lys Val
145 150 155 160

Gln Phe Arg Lys Pro Ala Pro Gly Ala Thr Asp Ala Val Pro Ser Arg
165 170 175

Lys Arg Ala Thr Pro Ile Asn Leu Ala Ser Ala Ile Arg Lys Ser Gly
180 185 190

Ala Ser Ala Val Ser Gly Gly Ser Gly Val Ser Gln Arg Pro Tyr Arg
195 200 205

Asp Arg Val Ile His Leu Leu Ala Leu Arg Pro Tyr Arg Lys Ala Glu
210 215 220

Leu Leu Leu Arg Leu Gln Lys Asp Gly Leu Thr Gln Ala Asp Lys Asp
225 230 235 240

Ala Leu Asp Gly Ile Leu Gln Gln Val Ala Asn Met Ser Ala Lys Asp
245 250 255

Gly Thr Cys Thr Leu Gln Asp Cys Met Tyr Lys Asp Val Gln Lys Asp

260 265 270
Trp Pro Gly Tyr Ser Glu Gly Asp Gln Gln Leu Leu Lys Arg Val Leu
275 280 285
Val Arg Lys Leu Cys Gln Pro Gln Ser Thr Gly Ser Leu Leu Gly Asp
290 295 300
Pro Ala Ala Ser Ser Pro Pro Gly Glu Arg Gly Arg Ser Ala Ser Pro
305 310 315 320
Pro Gln Lys Arg Leu Gln Pro Pro Leu Phe Ile Asp Pro Leu Ala Asn
325 330 335
Lys Lys Pro Arg Ile Ser His Phe Thr Gln Arg Ala Gln Pro Ala Val
340 345 350
Asn Gly Lys Leu Gly Val Pro Asn Gly Arg Glu Ala Leu Leu Pro Thr
355 360 365
Pro Gly Pro Pro Ala Ser Thr Asp Thr Leu Ser Ser Ser Thr His Leu
370 375 380
Pro Pro Arg Leu Glu Pro Pro Arg Ala His Asp Pro Leu Ala Asp Val
385 390 395 400
Ser Asn Asp Leu Gly His Ser Gly Arg Asp Cys Glu His Gly Glu Ala
405 410 415
Ala Ala Pro Ala Pro Thr Val Arg Leu Gly Leu Pro Leu Leu Thr Asp
420 425 430
Cys Ala Gln Pro Ser Arg Pro His Gly Ser Pro Ser Arg Ser Lys Pro
435 440 445
Lys Lys Lys Ser Lys Lys His Lys Asp Lys Glu Arg Ala Ala Glu Asp
450 455 460
Lys Pro Arg Ala Gln Leu Pro Asp Cys Ala Pro Ala Thr His Ala Thr
465 470 475 480
Pro Gly Ala Pro Ala Asp Thr Pro Gly Leu Asn Gly Thr Cys Ser Val
485 490 495
Ser Ser Val Pro Thr Ser Thr Ser Glu Thr Pro Asp Tyr Leu Leu Lys
500 505 510
Tyr Ala Ala Ile Ser Ser Ser Glu Gln Arg Gln Ser Tyr Lys Asn Asp
515 520 525
Phe Asn Ala Glu Tyr Ser Glu Tyr Arg Asp Leu His Ala Arg Ile Glu
530 535 540
Arg Ile Thr Arg Arg Phe Thr Gln Leu Asp Ala Gln Leu Arg Gln Leu
545 550 555 560
Ser Gln Gly Ser Glu Glu Tyr Glu Thr Thr Arg Gly Gln Ile Leu Gln
565 570 575
Glu Tyr Arg Lys Ile Lys Lys Thr Asn Thr Asn Tyr Ser Gln Glu Lys
580 585 590

His Arg Cys Glu Tyr Leu His Ser Lys Leu Ala His Ile Lys Arg Leu
595 600 605

Ile Ala Glu Tyr Asp Gln Arg Gln Leu Gln Ala Trp Pro
610 615 620

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 108 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asp Trp Ile Arg Glu Tyr Pro Pro Ile Thr Ser Asp Gln Gln Arg Gln
1 5 10 15

Leu Tyr Lys Arg Asn Phe Asp Thr Gly Leu Gln Glu Tyr Lys Ser Leu
20 25 30

Gln Ser Glu Leu Asp Glu Ile Asn Lys Glu Leu Ser Arg Leu Asp Lys
35 40 45

Glu Leu Asp Asp Tyr Arg Glu Glu Ser Glu Glu Tyr Met Ala Ala Ala
50 55 60

Asp Glu Tyr Asn Arg Leu Lys Gln Val Lys Gly Ser Ala Asp Tyr Lys
65 70 75 80

Ser Lys Lys Asn His Cys Lys Gln Leu Lys Ser Lys Leu Ser His Ile
85 90 95

Lys Lys Met Val Gly Asp Tyr Asp Arg Gln Lys Thr
100 105

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 297 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTCCACCGCT GCCTTCAACC TATCTGCCA TCTCACATCC TCCTCAGATT GTAAATTCTA 60
ACTCCAACTC CCCTAGCACT CCAGAAGGCC GGGGGACTCA AGACCTACCT GTTGACAGTT 120

TTAGTCAAAA CGATAGTATC TATGAGGACC AGCAAGACAA ATATACTCT AGGACTTCTC	180
TGGAAACCTT ACCCCCTGGT TCCGTTCTAC TAAAGTGTCC AAAGCCTATG GAAGAAAACC	240
ATTCAATGTC TCACAAAAAG TCCAAAAAGA AGTCTAAAAA ACATAAGGAA AAGGACC	297

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 358 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGCAACCGAA GCACAAAAGT TATCAAACCC GGTGGACCAT ATGTAGGGAA AAGAGTGCAA	60
ATTCGGAAAG CACCTCAAGC TGTTTCAGAT ACAGTTCTG AGAGGAAAAG GTCAACCCCC	120
ATGAACCTG CAAATACAAT TCGAAAGACA CATAGCAGCA GCACCATCTC TCAGAGGCCA	180
TACAGGGACA GGGTGATTCA NTTACTGGCC CTGAAGGCCT ACAAGAAACC GGAGCTACTT	240
GCTAGACTCC AGAAAGATGG TGTCAATCAA AAAGACAAGA ACTCCCTGGG GAGGCAATTN	300
TTGCAACAGG TAGNCCAATC TGGATTCTA AGGGACCTCT TCATATTACC TTTAAAGG	358

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 362 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGCGNCGTNN TCGNCGGGCA CCCCAGGGAG TTTGAAGATG GCGGCAGGGGG GGACAGGGGG	60
CCTNCAGGAG GAGCAGCGCT ATGGGCTGTC GTGCCGGACG GCTGGGGCAG GACAACATCA	120
CCGTACTGCA TGTNAAAGCT TCACCGAGAC GGNCGATTCC GGGGCGGTTG GAGAACCTAC	180
CAGAGCCACA AGNNNTTNAA TTCCCTTTTC GGACCTTCAA TCCAGTTCC AAGGACTCCA	240
CGGGCTTGT NCAAAAATTT CCCAAAAATG ATTCCCTTC AATGGANAGT TCATAAAATTT	300
TAAATTTTA ATTTGTTCAA ATNTTGGGGN AAAGNCAAAC CTTCAAGGGC NAGTTTGGA	360
CT	362

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 477 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AATTGGCAC GAGCATGGTC CTAGAACTCT GCTTNGACCA GAAGATGTGA ATAAACTTAA	60
GCTTATTTAT TTAAAATTCC AAATGAGTTN NTCTAGNTTC TAAAAAGGTG AAACCTTGCG	120
TGTTGAAAGT TTCAGTATTA GTAAACTTGA GTTACTTNN CTTTCCATT TNACTTGCT	180
TCCCTGCATT TCGAAGCTGC TCTTCTGGT CCTCCCCACC ACCCCACCCC CAAGACTTGT	240
GTTTGTAAAT AGAAATAATT TTTTAGGTA TTGGGGATCC ATTGTCTATT ATTCAAATC	300
AAGNTTTTN TTTNTCCTCA AAAANCTTGT GGTTTGTGA TTAGGAAATG GNNTTTTAG	360
ATATTGGGN TCCAGTGTCC NCACTTGAAA AGGTGGGNAG GGGTTAAAAA AANAGCANCA	420
GTAATNTGCA AGGTGNAATG NTTTGGTNA ACGGANGCCA TTTCCGACG TNCTTAA	477

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AAACATTCTC CAGCTCTGGG ACCTCCCANC TCAATTCCCT GGGATTNAT ACAAGATAAA	60
ATTACAGTGT GTGCACAAAC GACTCGTATC AAATGACACG AGAAANANTG ACCCAGGCAG	120
NGGAGGGAAT CCCGCAACCA ANGCACAAAA GTTATTCAAA CCCGGTGGGA CCATATNT	178

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GNCTTTCTC CANTCTAAA AGNGNTATCA CAATGTCAT GNAAGAAGTC TTACAAGAAT	60
ATCAGAAAGAT AAAGCCAGTC TAGTCCCAAT TACCATGAAG NAAAAATACA GATGTGNAAT	120
ATCTTCATAA CAAGCTGGCT CACATCAAAA GGCTAATN	158

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATAAAATAAGC TTAAGTTTAT TCACATCTTC TGGTCCAAGC AGAGTTCTAG GACCATGACT	60
CTGCTTGCTG TTGGTCAAAT TCACCTATTAA GCCTTTGAT GTGAGCCAGC TTGTTATGAA	120
GATATTTCACA TCTGTATTTT TCTTCATGGT AATTGGGACT AGACTGCTTT ATCTTCTGAT	180
ATTCTTGTAA GACTTCTTCA TGAACATTCT GATACTCTT TGAGCCTGGA GAAAGGCGCT	240
TTCTTTGTGC ATCTAGTTG ATAAATCTTC TAGCTACAGT CTCCATCCTG GCATGCAAAG	300
CTCTGTACTC ATCATACTCT GCATTGAAGT CATCCTTATA ATTCTGGCGT TGCTCATAGG	360
AGACGATAGC GATATATTTT ATCAAATAAT CTGGGAGTTC AATTGCTGAA GGGTCATGG	420
AGGCAGTGCA ATCCTCTT	438

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCGNCCGCAG TGGANGCTA GAGCGNAGCG CGCGGGCGCG GNCACCCCGG GGAGTTAAG	60
ATGGCGGCNG GGGGGACAGG GGGCCTGCGG GAGGAGCAGC GCTATGGGCT GTCGTGCGGA	120
CGGCTGGGGC AGGACAACAT CACCGTACTG CATGTGAAGC TCACCGAGAC GGCGATCCGG	180

GCGCTCGAGA CTTACCAGAG CCACAAGAAC TTAATTCCTT TTGACCTTC AATCCAGTTC	240
CAAGGACTCC ACGGGCTTGT CAAAATTCCC AAAAATGATC CCCTCAATGA AGTCATAAC	300
TTTAACCTTT ATTTGTCAAA TGTGGGCAA GACAACCCTC AGGGCAAGCT TTGACTGCAT	360
CCAGCAAACA TTCTCCAGCT CTGGAGCCTC CCAGCTCAAT TGCCTNGGGA TTTATACAAG	420
ATAAAATTAC AGTGTGTGCA ACAAACGACT CGTATCAGA	459

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 412 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TGGGATTCAA ATGACCATT AGTGTGGTG GTACTCTGTT CGTCAGGTGA GATATTGGG	60
CTTTTTTATT CATTAAAGGA TCAATAAACT CTGAATCCAA AAGCCGTTTC TGAGGAGAAG	120
ATACAGCATC TCTACTAGAA CATAcAGGAG ATTCTGAACG GCTGGTGCCT GTAGCATTCT	180
GAGACGGATT TAGTTTCTA GAGAGCACTG ACTCCAATGA CCGTCTGTCT ATTTCACTGT	240
ATCCAGGCCA GTCTCTTGA AGCTCTTAA AAACATAATC CTTAAGGGA TATGAGAGGT	300
CCTTAGAATT CAGATTGGCT AGCTGTTGCA GAATTGCTCC CAGGGAGTTC TTGTCTTTT	360
GATTGACACC ATCTTCTGG AGTCCTACAA GTAGCTCCGG GTTTCTTGTAA GG	412

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 487 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCAAATAAAAG AAACTTGACA TTGAGACCAT GGAGGAGAAC GAGGAAGACC TTCAGAGAGA	60
AGAAACTGCC AAGCTGAGTA ATGCCAGTCC AAATCCAAT GAAGGAGTTA AAGAAGGGTG	120
CACAGCCTCC ATGGAGCCTT CTTCAAGCACT TGAACCCCCA GATTATTTGA TAAAATATAT	180
TGCTATTGTC TCTTATGAGC AACGCCAGAA TTACAAGGAT GACTTCAATG CTGAGTATGA	240

TGAATACAGA GCTTGCATG CAAGGATGGA GACTGTAGCC AGGAGATTAA TTAAACTGGAA	300
TGCACAACGA AAACGCCCTT CTCCAGGTTC AAAAGAGTAC CAGAATGTTCA ATGAAGAAGT	360
CTTACAGGAA TATCAGAAGA TCAAGCAGTC CAGTCCAAT TACCATGAAG AAAAATACAG	420
ATGTGAATAT CTTCATAACA AGCTGGCTCA CATCAAAGAC TAATAGGTCG AATTTGACCA	480
ACAGCAA	487

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 525 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GCTTGCATG CCAGGATGGA GACTGTAGCT AGAAGATTAA TCAAACATAGA TGCACAAAGA	60
AAGGCCCTT CTCCAGGCTC AAAAGAGTAT CAGAATGTTCA ATGAAGAAGT CTTACAAGAA	120
TATCAGAAGA TAAAGCAGTC TAGTCCAAT TACCATGAAG AAAAATACAG ATGTGAATAT	180
CTTCATAACA AGCTGGCTCA CATCAAAGG CTAATAGGTG AATTTGACCA ACAGCAAGCA	240
GAGTCATGGT CCTAGAACTC TGCTTGACC AGAAGATGTG AATAAACTTA AGCTTATTAA	300
TTTAAAATTC CAAATGAGTT GCTCTAGATT CTAAAAAGGT GAAACTTGG CTGTTGAAAG	360
TTTCAGTATT AGTAAACTTN GAGTTACTTT TTCTTTCCA TTTTACTTTG CTTCCCTGCA	420
TTTCGGAAGC TGCCTCTTTN CTGGGTCTC NCCACTNGGG GCCAGCCCC AAGNACTTGG	480
TGTTTGGTT AATAGGNAAT AATTTCTTT AAGGGAATTG GGGGA	525

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 455 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTAGTCAAAA TGGTAGCATC TTTGAGGACC AGCAAGAAAA ATATACTCA AGGACTTGTC	60
TGGAAACATT ACCCCCCAGC TCAGCTCTGC TAAAGTGTCC AAAGCCCATG GAAGAAGAGC	120

ATCCAGTGTC TCACAAAAAG TCCAAAAGA AGTCTAAAAA ACACAAGGAA AAGGACCAAA	180
TAAAGAAACT TGACATTGAG ACCATGGAGG AGAAGGAGGA AGACCTTCAG AGAGAAGAAA	240
CTGCCAAGCT GAGTAATGCC AGTCCAATC CCAATGAAGG AGTTAAAGAA GGGTGCACAG	300
CCTCCATGGA GCCTTCTTCA GCACTTGAAC TCCCAGATTA TTTGATAAAA TATATTGCTA	360
TTGCTCTTA TGAGCAACGC CAGAATTACA AGGATGACTT CAATGCTGAG TATGATGAAT	420
ACAGAGCTTT GCATGCAAAGG ATGGAGACTG TAGCG	455

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 379 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TCACTTACTG GCCCTGAAGG CTACAAGAAA CCGGAGCTAC TTGCTAGACT CCAGAAAGAT	60
GGGTGTCATC AAAAAGACAA GAACTCCCTG GGAGCAATTG TGCAACAGGT AGCCAATCTG	120
AATTCTAAGG ACCTCTCAT A TACCTTAAAG GATTATGTTT TTAAAGAGCT TCAAAGAGAC	180
TGGCCTGGNT ACAGTGAAAT AGACAGACGG TCATTGGAGT CAGTGCTCTC TAGAAAAC	240
AATCCGTCTC AGAATGCTAC AGGCACCAGC CTNTCAGAAT CTCCTGTATG TTCTAGTAGA	300
GATGCTGTAT CTTCTCCTCA GGAAACGGCT TTTGGGTTTC AGAGTTTATT TGATCCCTT	360
AATGGANTTA AAAAAGGCT	379

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 519 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

NTCACTTACT GGCCCTGAAG CTANCAAGAA ACCGGAGCTA CTTGCTAGAC TCCAGAAAGA	60
TGGTGTCAAT CAAAAAGACA AGAACTCCCT GGGAGCAATT CTGCAACAGG TAGCCAATCT	120
GAATTCTAAG GACCTCTCAT ATACCTTAAA GGATTATGTT TTTAAAGAGC TTCAAAGAGA	180

CTGGCCTGGG ATACAGTGAA ATAGACAGAC GGTCAATTGGA GTCAGTGCTC TCTAGAAAAC	240
TAAATCCGTC TCAGAATGCT ACAGGCACCA GCGTTTCAGA ATCTCCTGTA TGTTCTAGTA	300
GGAGATGCTG TATCTTCTCC TCAGGAAACG GCTTTGGGT TCAGGAGTTT ATTTGATCCN	360
TTTAATGGAT TAAAAAAAGGC CCCGATTATT CTTCACCTGG ACGGAACAGA GTTACCNCCC	420
AACATTAATG GGTCCNTTG GATTCCCACC AGTGGAAAAT TGGGTGGCGG GCTTNCCCAT	480
TGCCCTGNG GGTGGTGGCN TTCCCCACCC TTNCACCGG	519

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 297 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GCTCCACCGCT GCCTTCAACC TATCTGCCA TCTCACATCC TCCTCAGATT GTAAATTCTA	60
ACTCCAACTC CCCTAGCACT CCAGAAGGCC GGGGGACTCA AGACCTACCT GTTGACAGTT	120
TTAGTCAAAA CGATAGTATC TATGAGGACC AGCAAGACAA ATATACTCT AGGACTTCTC	180
TGGAAACCTT ACCCCCTGGT TCCGTTCTAC TAAAGTGTCC AAAGCCTATG GAAGAAAACC	240
ATTCAATGTC TCACAAAAAG TCCAAAAAGA AGTCTAAAAA ACATAAGGAA AAGGACC	297

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 358 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CGCAACCGAA GCACAAAAGT TATCAAACCC GGTGGACCAT ATGTAGGGAA AAGAGTGCAA	60
ATTCGGAAAG CACCTCAAGC TGTTTCAGAT ACAGTTCTG AGAGGAAAAG GTCAACCCCC	120
ATGAACCCCTG CAAATACAAT TCGAAAGACA CATAGCAGCA GCACCATCTC TCAGAGGCCA	180
TACAGGGACA GGGTGATTCA NTTACTGGCC CTGAAGGCCT ACAAGAAACC GGAGCTACTT	240
GCTAGACTCC AGAAAGATGG TGTCAATCAA AAAGACAAGA ACTCCCTGGG GAGGCAATTN	300

TTGCAACAGG TAGNCCAATC TGGATTCTA AGGGACCTCT TCATATTACC TTTAAAGG 358

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 285 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TTTGTGAGA CATTGAATGG TTTCTTCCA TAGGCTTG AGACTTAGT AGAACGGAAC 60
CAGGGGGTAA GGTTCCAGA GAAGTCCTAG AGGTATATTT GTCTTGCTGG TCCTCATAGA 120
TACTATCGTT TTGACTAAAA CTNTCAACAG GTAGGTCTTG AGTCCCCCGG CCTTCTGGAG 180
TGCTAGGGGA GTTGGAGTTA GAATTTACAA TCTGAGGAGG ATGTGAGATG GGCAGATAGG 240
TTGAAGGCAG CGGTGGAGGG GTGGGGATGG CAGCAGCCCCA GGGGG 285

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 431 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TTTATTCCAA ACAGCATCAT CTACAACCTCA TAATCGCAGG CTCCTCCAGT TCATTTAAC 60
CAGAAAGCAG GCTTTTTCT CTTTCCCCT TTAAACAAAT GTAAAATACC TTCATTGGGA 120
TTGGACTGG CATTACTCAG CTTGGCAGTT TCTTCTCTCT GAAGGTCTTC CTCCTCTCC 180
TCCATGGTCT CAATGTCAAG TTTCTTTATT TGGTCCTTTT CCTTGTGTTT TTTAGACTTC 240
TTTTGGACT TTTGTGAGA CACTGGATGC TCTTCTTCCA TGGGCTTTGG ACACCTTAGC 300
AGAGTGAGCT GGGGGGTAAT GTTCCAGAC AAGTCCTTGA GGTATATTT TCTTGCTGGT 360
CCTCAAAGAT GCTACCATTT TGACTAAAAC TGTCAACAGG CAGGTCTTGA GTCCCAGGCC 420
TTCTGGAGTG C 431

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 196 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CACCGAGACG GCGATCCGGG CGCTCGAGAC TTACCAGAGC CACAAGAATT TAATTCTTT	60
TCGACCTTCA ATCCAGTTCC AAGGACTCCA CGGGCTTGTC AAAATTCCA AAAATGATCC	120
CCTCAATGAA GTTCATAACT TTAACCTTTA TTTGTCAAAT GTGGGCAAAG ACAACCCTCA	180
GGGGAGCTTG GGCTGC	196

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 197 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ACCATCTCTC AGAGGCCATA CAGGGACAGG GTGATTCACT TACTGGCCCT GAAGGCNTAC	60
AAGAAACCGG AGCTACTTGC TAGACTCCAG AAAGATGGTG TCAATCAAAA AGACAAGAAC	120
TCCCTGGGAG CAATTCTGCA ACAGGTAGCC AATCTGAATN CTAAGGACCT CNTCATATAC	180
CTTAAAGGAT TATGTTT	197

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GCGCCCGGCA GTGGAGGCTA GAGCCGCAGC GCGCGCGGG CGGACACCGC CGGGGAGGTT	60
TAAGAGTGGC GGCTGGGGGG GACAGGGGGG CCTGCAGGGA GGAGCAGCGC TATGGCTGT	120
CGTGCAGGACG GCGTGGGGCA GGACAACATC ACCGTACTGC ATGTGAAGCT CACCGAGACG	180

GCGATCCGGG CGCTCGAGAC TTACCAAGAGC CACAAGAATT TAATTCCCTT TCGACCTTCA	240
ATCCAGTTCC AAGGACTCCA CGGGGTGAGT ACTCTTATTG ATTTAACAAA CAAATCTAAT	300
GTTCTTGCAC GCTATTCAAC TTTAAAATC CGTTTCAGT TGACCCTT	348

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 184 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CGGAATTTTAA ATAAATAAGC TTAAGTTAT TCACATCTNC TGGTCCAAGC AGAGTTCTAG	60
GACCATGACT CTGCTTGCTG TTGGTCAAAT TCACCTATTA GCCTTNGAT GTGAGGCCAGC	120
TGTTATGAA GATATTACACA TCTGTATTT NCTTCATGGT AATTGGGACT AGACTGCTTT	180
ATCT	184

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 280 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TCCTAGAACT CTGCTTGGAC CAGAAGATGT GAATAAACTT AAGCTTATTT ATTTAAAATC	60
ACAAATGAGT TGCTCTAGAT TCTAAAAGGG TGAAACTTTG ACTGTTGAAA GTTTAAGTAT	120
TAGTAAACTT GAGTTACTTT TTCTTCAAA TTTCACTCCG CTTCCCTGCA TTTCGAAGCT	180
GCTCTTCTG GTCCTACCCA CCACCCCACC ACAAGACTT GTGTTGTTA ATAGAAATAA	240
TTTATCAAGG TATTGGGGAT CCATTGTCTA TATTTAAAAC	280

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 255 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

AACTAGCAGT CCCTTTGGGC CAATTGATGT AATTATTTTC AGTGTAAATC CNAAAGGTTG	60
CCTGTTTAN GNTAGGAGAT GATAGTAAAA ATACCTAATG CTCTGTTTT ATACCTCATA	120
CTAGGTAGCC AATCTGAATT CTAAGGACCT CTCATATACC TTAAAGGATT ATGTTNTAA	180
AGAGCTTCAA AGAGACTGGC CTGGATACAG TGAAATAGAC AGACGGTCAT TGGAGTCATG	240
TGCTCTCTAG GTGAA	255

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3974 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GGTACCTAAG TGAGTAGGGC GTCCGATCGA CGGACGCCCTT TTTTTGAAT TCGTAATCAT	60
GGTCATAGCT GTTCCCTGTG TGAAATTGTT ATCCGCTCAC AATTCCACAC AACATACGAG	120
CCGGAAGCAT AAAGTGAAA GCCTGGGTG CCTAATGAGT GAGCTAACTC ACATTAATTG	180
CGTTGCGCTC ACTGCCGCT TTCCAGTCGG GAAACCTGTC GTGCCAGCTG CATTAATGAA	240
TCGGCCAACG CGCGGGGAGA GGCGGTTGC GTATTGGCG CTCTTCCGCT TCCTCGCTCA	300
CTGACTCGCT GCGCTCGGTC GTTCGGCTGC GGCGAGCGGT ATCAGCTCAC TCAAAGGCGG	360
TAATACGGTT ATCCACAGAA TCAGGGATA ACGCAGGAAA GAACATGTGA GCAAAAGGCC	420
AGCAAAAGGC CAGGAACCGT AAAAAGGCCG CGTTGCTGGC GTTTTCCAT AGGCTCCGCC	480
CCCCTGACGA GCATCACAAA AATCGACGCT CAAGTCAGAG GTGGCGAAC CCGACAGGAC	540
TATAAAGATA CCAGGGCTTT CCCCTGGAA GCTCCCTCGT GCGCTCTCCT GTTCCGACCC	600
TGCCGCTTAC CGGATACCTG TCCGCCTTTC TCCCTCGGG AAGCGTGGCG CTTTCTCATA	660
GCTCACGCTG TAGGTATCTC AGTTGGTGT AGGTCGTTCG CTCCAAGCTG GGCTGTGTGC	720
ACGAACCCCC CGTTCAGCCC GACCGCTGCG CCTTATCCGG TAACTATCGT CTTGAGTCCA	780
ACCCGGTAAG ACACGACTTA TCGCCACTGG CAGCAGGCCAC TGGTAACAGG ATTAGCAGAG	840
CGAGGTATGT AGGCAGGTGCT ACAGAGTTCT TGAAGTGGTG GCCTAACTAC GGCTACACTA	900

GAAGAACAGT ATTTGGTATC TCGCCTCTGC TGAAGCCAGT TACCTTCGGA AAAAGAGTTG	960
GTAGCTCTTG ATCCGGCAAA CAAACCACCG CTGGTAGCGG TGGTTTTTT GTTGCAAGC	1020
AGCAGATTAC GCGCAGAAAA AAAGGATCTC AAGAAGATCC TTTGATCTTT TCTACGGGGT	1080
CTGACGCTCA GTGGAACGAA AACTCACGTT AAGGGATTT GGTCATGAGA TTATCGTCGA	1140
CAATT CGCGC GCGAAGGCAG AGCGGCATGC ATTTACGTTG ACACCATCGA ATGGTGAAA	1200
ACCTTCGCG GTATGGCATG ATAGCGCCCG GAAGAGAGTC AATTCAAGGGT GGTGAATGTG	1260
AAACCAGTAA CGTTATACGA TGTCGCAGAG TATGCCGGTG TCTCTTATCA GACC GTTCC	1320
CGCGTGGTGA ACCAGGCCAG CCACGTTCT GCGAAAACGC GGGAAAAAGT GGAAGCGGCG	1380
ATGGCGGAGC TGAATTACAT TCCCAACCAGC GTGGCACAAAC AACTGGCGGG CAAACAGTCG	1440
TTGCTGATTG GCGTTGCCAC CTCCAGTCTG GCCCTGCACG CGCCGTGCA AATTGTCGCG	1500
GCGATTAAAT CTCGCGCCGA TCAACTGGGT GCCAGCGTGG TGGTGTGAT GGTAGAACGA	1560
AGCGCGTCG AAGCCTGTAAGCAGCGGTG CACAATCTTC TCGCGCAACG CGTCAGTGGG	1620
CTGATCATTA ACTATCCGCT GGATGACCAG GATGCCATTG CTGTGGAAGC TGCCTGCACT	1680
AATGTTCCGG CGTTATTCT TGATGTCTCT GACCAGACAC CCATCAACAG TATTATTTTC	1740
TCCCATGAAG ACGGTACGCG ACTGGCGTG GAGCAGCTGG TCGCATTGGG TCACCAGCAA	1800
ATCGCGCTGT TAGCGGGCCC ATTAAGTTCT GTCTCGCGC GTCTCGTCT GGCTGGCTGG	1860
CATAAAATATC TCACTCGCAA TCAAATTCAAG CCGATAGCGG AACGGGAAGG CGACTGGAGT	1920
GCCATGTCCG GTTTCAACA AACCATGCAA ATGCTGAATG AGGGCATCGT TCCCAGTGC	1980
ATGCTGGTTG CCAACGATCA GATGGCGCTG GGCGCAATGC GCGCCATTAC CGAGTCCGGG	2040
CTGCGCGTTG GTGCGGATAT CTCGGTAGTG GGATACGACG ATACCGAAGA CAGCTCATGT	2100
TATATCCCGC CGTTAACAC CATCAAACAG GATTTCGCC TGCTGGGGCA AACCAGCGTG	2160
GACCGCTTGC TGCAACTCTC TCAGGGCCAG GCGGTGAAGG GCAATCAGCT GTTGCCTGTC	2220
TCACTGGTGA AAAGAAAAAC CACCCCTGGCG CCCAATACGC AAACCGCCTC TCCCCGCGCG	2280
TTGGCCGATT CATTAATGCA GCTGGCACGA CAGGTTCCCC GACTGGAAAG CGGGCAGTGA	2340
GCGCAACGCA ATTAATGTAA GTTAGCGCGA ATTGTGACCC AAAGCGGCCA TCGTGCCTCC	2400
CCACTCCTGC AGTCGGGGG CATGGATGCG CGGATAGCCG CTGCTGGTTT CCTGGATGCC	2460
GACGGATTG CACTGCCGGT AGAACTCCGC GAGGTCGTCC AGCCTCAGGC AGCAGCTGAA	2520
CCAACTCGCG AGGGGATCGA GCCCGGGGTG GCGAAGAAC TCCAGCATGA GATCCCCGCG	2580
CTGGAGGATC ATCCAGCCGG CGTCCCGGAA AACGATTCCG AAGCCCAACC TTTCATAGAA	2640
GGCGCGGGTG GAATCGAAAT CTCGTGATGG CAGGTTGGC GTCGCTGGT CGGTCAATTTC	2700
GAACCCCAGA GTCCCGCTCA GAAGAACCTCG TCAAGAAGGC GATAGAAGGC GATGCGCTGC	2760

GAATCGGGAG CGGGGATAACC GTAAAGCACG AGGAAGCGGT CAGCCCATTG GCCGCCAAGC	2820
TCTTCAGCAA TATCACGGGT AGCCAACGCT ATGTCCTGAT AGCGGTCCGC CACACCCAGC	2880
CGGCCACAGT CGATGAATCC AGAAAAGCGG CCATTTCCA CCATGATATT CGGCAAGCAG	2940
GCATGCCAT GGGTCACGAC GAGATCCTCG CCGTCGGGCA TGCGCGCCTT GAGCCTGGCG	3000
AACAGTTCGG CTGGCGCGAG CCCCTGATGC TCTTCGTCCA GATCATCCTG ATCGACAAGA	3060
CCGGCTTCCA TCCGAGTACG TGCTCGCTCG ATGCGATGTT TCGCTTGGTG GTCGAATGGG	3120
CAGGTAGCCG GATCAAGCGT ATGCAGCCGC CGCATTGCAT CAGCCATGAT GGATACTTTC	3180
TCGGCAGGAG CAAGGTGAGA TGACAGGAGA TCCTGCCCCG GCACCTCGCC CAATAGCAGC	3240
CAGTCCCTTC CCGCTTCAGT GACAACGTGG AGCACAGCTG CGCAAGGAAC GCCCGTCGTG	3300
GCCAGGCCACG ATAGCCGCGC TGCCCTCGTCC TGCAAGTTCAT TCAGGGCACC GGACAGGTG	3360
GTCTTGACAA AAAGAACCGG GCGCCCCCTGC GCTGACAGCC GGAACACGGC GGCATCAGAG	3420
CAGCCGATTG TCTGTTGTGC CCAGTCATAG CCGAATAGCC TCTCCACCCA AGCGGCCGGA	3480
GAACCTGCGT GCAATCCATC TTGTTCAATC ATGCGAAACG ATCCTCATCC TGTCTTTGA	3540
TCAGATCTTG ATCCCCCTGCG CCATCAGATC CTTGGCGGCA AGAAAGCCAT CCAGTTTACT	3600
TTGCAGGGCT TCCCAACCTT ACCAGAGGGC GCCCCAGCTG GCAATTCCGG TTCGCTTGCT	3660
GTCCATAAAA CCGCCCAGTC TAGCTATCGC CATGTAAGCC CACTGCAAGC TACCTGCTTT	3720
CTCTTGCGC TTGCGTTTTC CCTTGTCCAG ATAGCCCAGT AGCTGACATT CATCCGGGGT	3780
CAGCACCGTT TCTGCGGACT GGCTTCTAC GTGTTCCGCT TCCTTAGCA GCCCTTGC	3840
CCTGAGTGCT TGCAGCAGCG TGAAGCTTAA AAAACTGCAA AAAATAGTTT GACTTGTGAG	3900
CGGATAACAA TTAAGATGTA CCCAATTGTG AGCGGATAAC AATTCACAC ATTAAAGAGG	3960
AGAAATTACA TATG	3974

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AAGCTTAAAA AACTGCAAAA AATAGTTGA CTTGTGAGCG GATAACAATT AAGATGTACC	60
CAATTGTGAG CGGATAACAA TTTCACACAT TAAAGAGGAG AAATTACATA TG	112